length or, preferably from about 10 to 50 base pairs in length or, more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, and potential for formation of loops and other factors, which are well known in the art. Tools and software suitable for designing probes, and especially suitable for designing PCR primers, are available on the Internet, for example. A software program suitable for designing probes, and especially for designing PCR primers, is available from Premier Biosoft International, 3786 Corina Way, Palo Alto, CA 94303-4504. Preferred techniques for designing PCR primers are also disclosed in Dieffenbach and Dyksler, *PCR primer: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1995.--

B6 cont.

On page 42, line 2, replace the present title with the following new title:

B7 --POLYNUCLEOTIDES FOR USE IN THE MODIFICATION OF GENE TRANSCRIPTION--

IN THE CLAIMS:

Cancel claim 30.

Amend claims 2 and 33 as follows:

B8 2. (Twice Amended) An oligonucleotide probe or primer comprising at least 20 contiguous residues complementary to 20 contiguous residues of SEQ ID NO: 2076.

33. (Amended) An isolated polynucleotide comprising a sequence selected from the group consisting of:

B9 sub C1

(a) sequences that are degeneratively equivalent to SEQ ID NO: 2076;

(b) sequences having at least 75% identity to SEQ ID NO: 2076;

(c) sequences having at least 90% identity to SEQ ID NO: 2076; and

(d) sequences having at least 95% identify to SEQ ID NO: 2076,

wherein the polynucleotide encodes a Myb transcription factor.

Add the following new claim:

B10 --35. An isolated polynucleotide that encodes SEQ ID NO: 2249.--